



STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/559,434
Source: PCT 10
Date Processed by STIC: 12/16/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/web/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/559,434

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.~~
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

08159

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/559,434DATE: 12/16/2005
TIME: 15:38:57Input Set : A:\SEQUENCE LISTING.txt
Output Set : N:\CRF4\12162005\J559434.raw

3 <110> APPLICANT: Degussa AG
5 <120> TITLE OF INVENTION: Screening process for hydantoin racemases
7 <130> FILE REFERENCE: 030115 AM
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,434
C--> 10 <141> CURRENT FILING DATE: 2005-12-05
12 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed
Cp9-1, 2, 3, 4, 5

ERRORED SEQUENCES

156 <210> SEQ ID NO: 4
157 <211> LENGTH: 237 → found 236
158 <212> TYPE: PRT
159 <213> ORGANISM: Artificial sequence
W--> 160
160 <223> OTHER INFORMATION: Description of the artificial sequence (1BG7)
162 <400> SEQUENCE: 4
163 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
164 1 5 10 15
166 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
167 20 25 30
169 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
170 35 40 45
172 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
173 50 55 60
175 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp
176 65 70 75 80
178 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
179 85 90 95
181 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
182 100 105 110
184 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
185 115 120 125
187 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
188 130 135 140
190 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
191 145 150 155 160
193 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
194 165 170 175
196 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
197 180 185 190
199 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys

Mandatory field
identifier is missing.
Pls Insert.

Invalid Response.
What is the
Source of genetic
Material?
Pls see item
11 on
Error Summary
Sheet.

<210> 1
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence
 Consensus sequence

<400> 1
 Phe Xaa Asp Xaa Gly Leu
 1 5

Pls Explain 'Xaa' locations which
 residue they represents.
 See Error Explanation on page-6

RY1

Some of errors shown exist throughout
 the Listing. Please check subsequent
 sequences for similar errors.

See pg 10 of the app

Phe X₁ Asp X₂ GL

~~X₂ = Asp~~ X₁ = Ser 10

X₂ = P or T

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005
TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12162005\J559434.raw

```

200          195          200          205
202 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
203          210          215          220
205 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 206 225          230          235
283 <210> SEQ ID NO: 6
284 <211> LENGTH: 237
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial sequence
W--> 287 <223> OTHER INFORMATION: Description of the artificial sequence: 3CH11
E--> 289 <400> SEQUENCE: 6
290 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
291 1 5 10 15
293 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
294 20 25 30
296 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
297 35 40 45
299 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
300 50 55 60
302 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Glu Asp
303 65 70 75 80
305 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
306 85 90 95
308 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
309 100 105 110
311 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
312 115 120 125
314 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
315 130 135 140
317 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
318 145 150 155 160
320 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
321 165 170 175
323 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
324 180 185 190
326 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
327 195 200 205
329 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
330 210 215 220
332 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 333 225          230          235
412 <210> SEQ ID NO: 8
413 <211> LENGTH: 237
414 <212> TYPE: PRT
415 <213> ORGANISM: Artificial sequence
W--> 416 <223> OTHER INFORMATION: Description of the artificial sequence: AE3
418 <400> SEQUENCE: 8

```

found 236

Insert <220>

Same Error

pls Insert <220>

Same Error